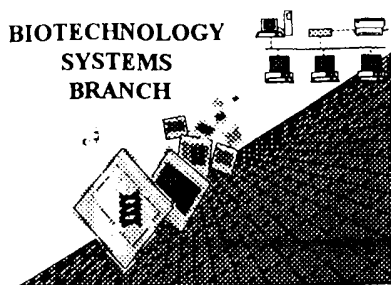


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



A 5

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/831,951

Source: Pur/09

Date Processed by STIC: 9/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,951

DATE: 09/05/2001

TIME: 13:21:11

Input Set : A:\Osanaï Seq Lst 8-14-01.txt

Output Set: N:\CRF3\09052001\I831951.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Osanaï, Tomohiro
 2 Magota, Koji
 W--> 3 <120> TITLE OF INVENTION: Inhibitor and Activator of Coupling Factor-6 and Antigen thereto
 W--> 4 <130> FILE REFERENCE: 46220
 W--> 5 <140> CURRENT APPLICATION NUMBER: US 09/831,951
 6 <141> CURRENT FILING DATE: 2001-05-16
 7 <150> PRIOR APPLICATION NUMBER: JPA 264687/99
 8 <151> PRIOR FILING DATE: 1999-09-17
 W--> 9 <160> NUMBER OF SEQ ID: 24

pp 1-2

ERRORED SEQUENCES

117 <210> SEQ ID NO: 6
 118 <211> LENGTH: 23
 119 <212> TYPE: DNA
 120 <213> ORGANISM: Artificial Sequence
 W--> 121 <220> FEATURE:
 W--> 122 <221> NAME/KEY:
 123 <222> LOCATION:
 124 <223> OTHER INFORMATION: Primer used in PCR method
 W--> 125 <400> SEQUENCE: 6
 E--> 126 atgactgttc agaggatctt cag
 129 <210> SEQ ID NO: 7
 130 <211> LENGTH: 27
 131 <212> TYPE: DNA
 132 <213> ORGANISM: Artificial Sequence
 W--> 133 <220> FEATURE:
 W--> 134 <221> NAME/KEY:
 135 <222> LOCATION:
 136 <223> OTHER INFORMATION: Primer used in PCR method
 W--> 137 <400> SEQUENCE: 7
 E--> 138 gtcgactcag gactgggggtt tgctcag
 141 <210> SEQ ID NO: 8
 142 <211> LENGTH: 33
 143 <212> TYPE: DNA
 144 <213> ORGANISM: Artificial Sequence
 W--> 145 <220> FEATURE:
 W--> 146 <221> NAME/KEY:
 147 <222> LOCATION:
 148 <223> OTHER INFORMATION: Primer used in PCR method
 W--> 149 <400> SEQUENCE: 8
 E--> 150 atgattcttc agaggctctt cag
 153 <210> SEQ ID NO: 9
 154 <211> LENGTH: 28
 155 <212> TYPE: DNA
 156 <213> ORGANISM: Artificial Sequence

*23 ← insert cumulative base
 total at right margin
 of each line*

27 ← insert

23 ←

RAW SEQUENCE LISTING

DATE: 09/05/2001

PATENT APPLICATION: US/09/831,951

TIME: 13:21:11

Input Set : A:\Osana1 Seq Lst 8-14-01.txt

Output Set: N:\CRF3\09052001\I831951.raw

W--> 157 <220> FEATURE:
W--> 158 <221> NAME/KEY:
159 <222> LOCATION:
160 <223> OTHER INFORMATION: Primer used in PCR method
W--> 161 <400> SEQUENCE: 9
E--> 162 gtcgactcag gcttggggtt tttcgatg 28 ←
165 <210> SEQ ID NO: 10
166 <211> LENGTH: 45
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
W--> 169 <220> FEATURE:
W--> 170 <221> NAME/KEY:
171 <222> LOCATION:
172 <223> OTHER INFORMATION: Gene coding for enterokinase recognition site and Eco RI recognition
173 site
W--> 174 <400> SEQUENCE: 10
E--> 175 gaattcgacg atgacgataa gaataaggaa cttgatcctg tacag 45 ←
178 <210> SEQ ID NO: 11
179 <211> LENGTH: 46
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
W--> 182 <220> FEATURE:
W--> 183 <221> NAME/KEY:
184 <222> LOCATION:
185 <223> OTHER INFORMATION: Gene coding for enterokinase recognition site and Eco RI recognition.
186 site
W--> 187 <400> SEQUENCE: 11
E--> 188 gaattcgacg atgacgataa gaataaggaa cttgatccta tacaga 46 ←
191 <210> SEQ ID NO: 22
192 <211> LENGTH: 31
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
W--> 199 <220> FEATURE:
W--> 200 <221> NAME/KEY:
201 <222> LOCATION:
202 <223> OTHER INFORMATION: Primer for PCR method
W--> 203 <400> SEQUENCE: 22
E--> 204 gatcgaggga gtaataagggaacttgatcct
207 <210> SEQ ID NO: 23
208 <211> LENGTH: 26
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
W--> 211 <220> FEATURE:
W--> 212 <221> NAME/KEY:
213 <222> LOCATION:
214 <223> OTHER INFORMATION: Primer for PCR method
W--> 215 <400> SEQUENCE: 23
E--> 216 gtcgacttaggactggggtttgtcga 26

separate into groups of 10

[illegible]

TIME: 1:01:12

Input Set : A:\Osanai Seq Lst 8-14-01.txt

Output Det: N:\CRF3\09052001\I831951.raw

```

L:1 M:282 W: Missing Blank Line separator, <120> field identifier
L:1 M:282 W: Missing Blank Line separator, <130> field identifier
L:1 M:282 W: Missing Blank Line separator, <140> field identifier
L:1 M:282 W: Missing Blank Line separator, <150> field identifier
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:3 M:283 W: Missing Blank Line separator, <400> field identifier
L:6 M:283 W: Missing Blank Line separator, <220> field identifier
L:6 M:287 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#3
L:6 M:283 W: Missing Blank Line separator, <400> field identifier
L:14 M:2-3 W: Missing Blank Line separator, <400> field identifier
L:100 M:182 W: Missing Blank Line separator, <400> field identifier
L:111 M:182 W: Missing Blank Line separator, <220> field identifier
L:111 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#6
L:111 M:183 W: Missing Blank Line separator, <400> field identifier
L:116 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:116 M:183 W: Missing Blank Line separator, <220> field identifier
L:116 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#7
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:7
L:118 M:183 W: Missing Blank Line separator, <220> field identifier
L:118 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#8
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:8
L:117 M:183 W: Missing Blank Line separator, <220> field identifier
L:117 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#9
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:9
L:118 M:183 W: Missing Blank Line separator, <220> field identifier
L:117 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#10
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:10
L:118 M:183 W: Missing Blank Line separator, <220> field identifier
L:118 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#11
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:11
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <400> field identifier
L:117 M:183 W: Missing Blank Line separator, <220> field identifier
L:117 M:187 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#21
L:118 M:183 W: Missing Blank Line separator, <400> field identifier
L:118 M:183 W: Missing Blank Line separator, <220> field identifier

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,951

DATE: 04/20/01

TIME: 11:21:11

Input Set : A:\Osana1 Seq Lst 8-14-01.txt

Output Set: N:\CRF3\09052001\I831951.raw

L:300 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:303 M:283 W: Missing Blank Line separator, <4> field identifier
L:304 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:22
L:311 M:283 W: Missing Blank Line separator, <220> field identifier
L:312 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:315 M:283 W: Missing Blank Line separator, <4> field identifier
L:316 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:23
L:323 M:283 W: Missing Blank Line separator, <220> field identifier
L:324 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:327 M:283 W: Missing Blank Line separator, <4> field identifier